



SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: KAUFMAN, RUSSEL E.
SLENTZ-KESLER, KIMBERLY
- (ii) TITLE OF INVENTION: GENE PRODUCT OVER EXPRESSED IN CANCER
CELLS
- (iii) NUMBER OF SEQUENCES: 2
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: NIXON & VANDERHYE P.C.
 - (B) STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
 - (C) CITY: ARLINGTON
 - (D) STATE: VIRGINIA
 - (E) COUNTRY: U.S.A.
 - (F) ZIP: 22201-4714
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 10/080,522
 - (B) FILING DATE: 25-FEB-2002
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 09/539,774
 - (B) FILING DATE: 31-MAR-2000
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 09/210,474
 - (B) FILING DATE: 14-DEC-1998
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/755,559
 - (B) FILING DATE: 22-NOV-1996
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: WILSON, MARY J.
 - (B) REGISTRATION NUMBER: 32,955
 - (C) REFERENCE/DOCKET NUMBER: 1579-645
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (703) 816-4000
 - (B) TELEFAX: (703) 816-4100

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 248 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met	Gln	Thr	Cys	Pro	Leu	Ala	Phe	Pro	Gly	His	Val	Ser	Gln	Ala	Leu
1				5					10					15	
Gly	Thr	Leu	Leu	Phe	Leu	Ala	Ala	Ser	Leu	Ser	Ala	Gln	Asn	Glu	Gly
		20						25					30		
Trp	Asp	Ser	Pro	Ile	Cys	Thr	Glu	Gly	Val	Val	Ser	Val	Ser	Trp	Gly
		35					40					45			
Glu	Asn	Thr	Val	Met	Ser	Cys	Asn	Ile	Ser	Asn	Ala	Phe	Ser	His	Val
	50					55					60				
Asn	Ile	Lys	Leu	Arg	Ala	His	Gly	Gln	Glu	Ser	Ala	Ile	Phe	Asn	Glu
65					70					75					80
Val	Ala	Pro	Gly	Tyr	Phe	Ser	Arg	Asp	Gly	Trp	Gln	Leu	Gln	Val	Gln
				85					90					95	
Gly	Gly	Val	Ala	Gln	Leu	Val	Ile	Lys	Gly	Ala	Arg	Asp	Ser	His	Ala
			100					105					110		
Gly	Leu	Tyr	Met	Trp	His	Leu	Val	Gly	His	Gln	Arg	Asn	Asn	Arg	Gln
		115					120					125			
Val	Thr	Leu	Glu	Val	Ser	Gly	Ala	Glu	Pro	Gln	Ser	Ala	Pro	Asp	Thr
	130					135					140				
Gly	Phe	Trp	Pro	Val	Pro	Ala	Val	Val	Thr	Ala	Val	Phe	Ile	Leu	Leu
145					150					155					160
Val	Ala	Leu	Val	Met	Phe	Ala	Trp	Tyr	Arg	Cys	Arg	Cys	Ser	Gln	Gln
				165					170					175	
Arg	Arg	Glu	Lys	Lys	Phe	Phe	Leu	Leu	Glu	Pro	Gln	Met	Lys	Val	Ala
			180					185					190		
Ala	Leu	Arg	Ala	Gly	Ala	Gln	Gln	Gly	Leu	Ser	Arg	Ala	Ser	Ala	Glu
		195					200					205			
Leu	Trp	Thr	Pro	Asp	Ser	Glu	Pro	Thr	Pro	Arg	Pro	Leu	Ala	Leu	Val
	210					215					220				
Phe	Lys	Pro	Ser	Pro	Leu	Gly	Ala	Leu	Glu	Leu	Leu	Ser	Pro	Gln	Pro
225					230					235					240
Leu	Phe	Pro	Tyr	Ala	Ala	Asp	Pro								
					245										

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2180 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATTCTGCTT CCTTTAGCGT GAACGCGGGT GCGGTGCCTC CCGTGAAATA ATAAATTCAC	60
CGTCACGCTT GTTGTGAACG CGGGTGGTTC CCGAAACTTG GAGGCTTCCC GTAAACCCAG	120
CTCCTTCCTC ATCTGGGAGG TGGGTCCCGC GCGGGTCCGC CGCCTCCTCC CTGGCCCCCTC	180
CCTCTCGTGT CTTTCATTTT CCTGGGGCTC CGGGGCGCGG AGAAGCTGCA TCCCAGAGGA	240
GCGCGTCCAG GAGCGGACCC GGGAGTGTTT CAAGAGCCAG TGACAAGGAC CAGGGGCCCA	300
AGTCCCACCA GCCATGCAGA CCTGCCCCCT GGCATTCCCT GGCCACGTTT CCCAGGCCCT	360
TGGGACCCTC CTGTTTTTGG CTGCCTCCTT GAGTGCTCAG AATGAAGGCT GGGACAGCCC	420
CATCTGCACA GAGGGGGTAG TCTCTGTGTC TTGGGGCGAG AACACCGTCA TGTCTGCAA	480
CATCTCCAAC GCCTTCTCCC ATGTCAACAT CAAGCTGCGT GCCCACGGGC AGGAGAGCGC	540
CATCTTCAAT GAGGTGGCTC CAGGCTACTT CTCCCGGGAC GGCTGGCAGC TCCAGGTTCA	600
GGGAGGCGTG GCACAGCTGG TGATCAAAGG CGCCCGGGAC TCCCATGCTG GGCTGTACAT	660
GTGGCACCTC GTGGGACACC AGAGAAATAA CAGACAAGTC ACGCTGGAGG TTTAGGTGC	720
AGAACCCCAG TCCGCCCTG AACTGGGT CTGGCCTGTG CCAGCGGTGG TCACTGCTGT	780
CTTCATCCTC TTGGTCGCTC TGGTCATGTT CGCCTGGTAC AGGTGCCGCT GTTCCCAGCA	840
ACGCCGGGAG AAGAAGTTCT TCCTCCTAGA ACCCCAGATG AAGGTCGCAG CCCTCAGAGC	900
GGGAGCCCAG CAGGGCCTGA GCAGAGCCTC CGCTGAACTG TGGACCCCAG ACTCCGAGCC	960
CACCCCAAGG CCGCTGGCAC TGGTGTTCAA ACCCTCACCA CTTGGAGCCC TGGAGCTGCT	1020
GTCCCCCCCA ACCCTTGTTT CCATATGCCG CAGACCCATA GCCGCCTGCA AGGCAGAGAG	1080
GACACAGGAG AGCCAGCCCT GAGTGCCGAC CTTGGGTGGC GGGGCCCTGG TCTCTCGTCC	1140
CACCCGAGG GCACAGACAC CGGCTTGCTT GGCAGGCTGG GCCTCTGTGT CACCCACTCC	1200
TGGGTGCGTG CAGACCTTC CCCTCCACCC CCCAGGTCTT CCAAGCTCTG CTTCCTCAGT	1260
TTCCAAAATG GAACCACCTC ACCTCCGCAG CACCCGACTT ACCAGGACGC ATGCCCCCTCC	1320
CTCTGCCCTC ATCAAACCCA CAGACCCGGA CTCCCTTTCT GCCACCCAG GCTGGTCCGG	1380
CCCCAGGTGT GGGGTCCGCT CTCTCCACTC CCAGGGCTCC GCGCCCAAGT GAGGGGGCCC	1440
CTGCCGGAGC CTCAGACACA CTGGAGTTCA GGGCTGGGGG GGCCTTGGCA CATACTGTC	1500
CCTTGGCTAT GAGCAGGCTT TGGGGGCCCT TCCGCGCAG CCCCAGGGGC CGAGGTAGGG	1560
TCTGGGGGCT TAGAGGCTGG GATGGCTCCT GGCCCCACCG CCAGGGGGCA AGCGCAGGCC	1620
GGGCTGGGAG GCGGCGGCGG CGGCTCGGGC TGGGGGGTCA GGTGGACGCT GCCTCCGGGG	1680
CTGGTCGCGC ATCCCTCAGT CCCTCGGCCA CCCGGGGGTC GCTCCCTCGT GCCCACCGCA	1740

CCTGCCGAGC	CTCTTTGGAC	CCAGATCTGT	TCATGCTTTT	GTCTTCGTCA	CTGCGGCGGG	1800
GCCCTTTGAT	GTCTTCATCT	GTATGGGGTG	GAAAAATCAC	CGGGAATCCC	CCTTCAGTTC	1860
TTTGAAAAAG	TTCCATGACT	CGAATATCTG	AAATGAAGAA	AACAAACCGA	CTCACAAACC	1920
TCCAAGTAGC	TCCAAATGCA	ATTTTTTAAA	TGGAAAACAA	AAATCTGAAA	GAAACGTCTT	1980
TAGTGGCTTT	AAGCCCCAAA	ACGTCCCTAA	GGCGTCCTCG	AGATGAAGAC	GGGGGGGAGC	2040
CCCAGCCAGG	TGGAGACCCC	GCAGGACGCG	GCGGCGCCCG	GTGACCGAGG	CCTCGCACAG	2100
CCGGCCGCCC	TGAGGGTCGG	GCCGAGCCAG	GGTCCAAGAG	GGGCGCGTTT	GTGTCTCGGG	2160
TTAAAATAAG	GTTCCGTCCG					2180